

Remarks:

Claim 30 has been amended to replace the term "crystallizable" with "crystallized." Support for this claim amendment can be found, *e.g.*, in original claim 1, paragraph 11, 107-111 and 125 of the application. Upon entry of this amendment and response, claims 1-12, 29-32 and 35 are elected for further prosecution, and claims 13-28, 33-34 and 36-39 are withdrawn. No new matter has been added.

Applicants note that representation of this application has been recently transferred to Fish & Richardson from the previous representative. A Revocation and New Power of Attorney document will be submitted to the Office shortly.

In the Restriction Requirement mailed July 12, 2007, the claims of the above-identified patent application were restricted as follows:

Group I: Claims 1-12, 29-32 and 35, drawn to a crystal comprising at least 150 amino acid residues of the LXR β ligand binding domain, and an isolated protein consisting essentially of the amino acid sequence shown from amino acid sequence 220 to amino acid 461 in FIG. 5a (SEQ ID NO: 1) or the sequence shown in FIG. 5b (SEQ ID NO:2).

Group II: Claims 13-19 and 21-28, drawn to a drug screening assay comprising the steps of (a) selecting a potential ligand by performing rational drug design with the three-dimensional structure determined for the crystal of claim 1, wherein said selecting is performed in conjunction with computer modeling; (b) contacting (*i.e.*, docking) the potential ligand with the ligand binding domain of LXR β ; and (c) detecting the binding of the potential ligand for the ligand binding domain.

Group III: Claims 20, 36 and 37, drawn to a machine-readable data storage medium, comprising a data storage material encoded with machine readable data which, using a machine programmed with instructions for using said data, is capable of displaying a graphical three-dimensional representation of a crystal structure according to claim 1 or a homologue of said crystal structure.

Group IV: Claims 33 and 34, drawn to a vector, such as a plasmid, containing a nucleic acid molecule encoding a protein consisting of the amino acid sequence shown from 220 to 461 in FIG. 5a (SEQ ID NO: 1) or the sequence shown in FIG. 5b (SEQ ID NO: 2); and a host cell containing a vector according to claim 33.

Group V: Claims 38 and 39, drawn to a method for determining the three-dimensional structure of a complex of a complex between LXR β and a ligand therefore, which comprises: (a) obtaining x-ray diffraction data for crystals of the complex as defined in claim 1; and (b) utilizing a set of atomic coordinates as defined in claim 29 or a portion thereof; and coordinates having a root mean square deviation therefrom with respect to conserved protein backbone atoms of not more than 1.5 angstrom to define the three-dimensional structure of the complex.

Applicants hereby elect without traverse to prosecute the claims of **Group I, claims 1-12, 29-32 and 35**. The non-elected claims are withdrawn from consideration. Applicants reserve the right to file one or more divisional applications directed to the unelected claims pursuant to 35 USC §§120 and 121.

Species Election

In addition to the above election, the Office requested the Applicants to elect a single SEQ ID NO, selected from SEQ ID NO: 2, SEQ ID NO: 4 and SEQ ID NO: 6. Additionally, the Office also requested the Applicants elect a single cysteine position from the list in claim 11 for the corresponding SEQ ID No. elected above.

Applicants thank the Examiner for discussing the species election with Applicants' previous attorney, Elizabeth Galletta on August 10, 2007. Per that interview, the Examiner stated the species election with regard to the SEQ ID NO. should have referred to SEQ ID NO: 1 or SEQ ID NO:2, instead of SEQ ID NO:2, SEQ ID NO:4 and SEQ ID NO:6. Accordingly, Applicants herein elect SEQ ID NO:1 as the species for purposes of examination. The elected claims read on the elected species. The Office is reminded to follow the procedure in MPEP 803.02 and to extend the search to the other species recited in the claims should the elected

species be free of the prior art. It is noted that SEQ ID NO:2 corresponds to the crystallized human LXR β sequence having amino acids 213-416 from SEQ ID NO:1 fused to four non-LXR beta residues, Gly-Ser-His-Met-, fused at the N-terminus.

Additionally, during the August 10 interview, the Examiner appears to have noted that the species election regarding the cysteine position was in error, and therefore the Applicants may disregard this species election.

However, during the interview, the Examiner appears to have inquired about the sequence listing associated with claims 8-10. Applicants submit that claims 8-10 are directed to crystals of LXR β belonging to specific space groups and having specific unit cell dimensions. The structural features required by these claims are set forth by specifying the space groups and unit cell dimensions. Thus, no explicit reference to a SEQ ID NO is necessary to comply with the written description and enablement requirements.

Additionally, the Examiner appears to have inquired about the atomic coordinates provided on pages 28-357. Applicants submit this data discloses a polypeptide sequence of SEQ ID NO: 1, which comprises a ligand binding domain starting at Leu 220 until the C-terminus. The sequence included in the atomic coordinate is disclosed in the Sequence Listing submitted on July 21, 2006 and disclosed in Figs. 5a and 5b. Accordingly, Applicants submit a new Sequence Listing is not required.

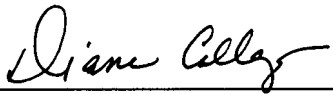
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Respectfully submitted,

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